

0250

#6

OIEP

ENTERED

RAW SEQUENCE LISTING

DATE: 06/19/2000

PATENT APPLICATION: US/09/589,510

TIME: 12:11:54

Input Set : A:\1121SEQLIST.TXT

Output Set: N:\CRF3\06192000\I589510.raw

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4 <110> APPLICANT: Mahajan, Pramod B.
6 <120> TITLE OF INVENTION: Maize Orthologues of Bacterial RuvB:
7   cDNAs and Uses Thereof
9 <130> FILE REFERENCE: 1121
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/589,510
C--> 11 <141> CURRENT FILING DATE: 2000-06-07
11 <150> PRIOR APPLICATION NUMBER: US 60/144,112
12 <151> PRIOR FILING DATE: 1999-07-16
14 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1845
20 <212> TYPE: DNA
21 <213> ORGANISM: Zea mays
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (85)...(1449)
27 <400> SEQUENCE: 1
28   gacccacgcg tcgcccaccc cccgccccca aattttggca gctccacaga aacagagagc   60
29   gcataaccgg cggtgttggc ggcgatg agg atc gag gag gtg cag tcg acc   111
30                                     Met Arg Ile Glu Glu Val Gln Ser Thr
31                                     1           5
33   tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga ctc ggc   159
34   Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly
35   10           15           20           25
37   ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc gtg ggc   207
38   Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe Val Gly
39   30           35           40
41   cag tcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg att cgc   255
42   Gln Ser Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg
43   45           50           55
45   cag aaa aag atg gcc ggc cgc gcg gtg ctc ctt gtg ggt ccg ccc gcc   303
46   Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala
47   60           65           70
49   acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc ggc agc   351
50   Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser
51   75           80           85
53   aag gtc cct ttc tgc cct atg gta gga tca gaa gtg tac tcc tcg gag   399
54   Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu
55   90           95           100           105
57   gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct ata ggt   447
58   Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly
59   110           115           120
61   ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt act gaa   495
62   Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Thr Glu
63   125           130           135
65   ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca aaa agc   543

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66	Leu	Ser	Pro	Glu	Glu	Ala	Glu	Ser	Thr	Thr	Gly	Gly	Tyr	Ala	Lys	Ser	
67			140				145						150				
69	att	agc	cat	gta	atc	atc	agc	tta	aag	act	gtt	aaa	ggg	act	aag	caa	591
70	Ile	Ser	His	Val	Ile	Ile	Ser	Leu	Lys	Thr	Val	Lys	Gly	Thr	Lys	Gln	
71			155				160						165				
73	ctg	aag	tta	gat	tct	tca	att	tat	gat	gct	ctg	atc	aag	gaa	aag	gtg	639
74	Leu	Lys	Leu	Asp	Ser	Ser	Ile	Tyr	Asp	Ala	Leu	Ile	Lys	Glu	Lys	Val	
75			170				175				180						
77	gca	gtg	ggt	gat	gtt	ata	tac	att	gaa	gca	aat	agt	gga	gca	gtg	aaa	687
78	Ala	Val	Gly	Asp	Val	Ile	Tyr	Ile	Glu	Ala	Asn	Ser	Gly	Ala	Val	Lys	
79				190							195				200		
81	aga	gtt	ggt	aga	tgt	gat	tct	ttt	gct	aca	gaa	tac	gat	ctt	gaa	gct	735
82	Arg	Val	Gly	Arg	Cys	Asp	Ser	Phe	Ala	Thr	Glu	Tyr	Asp	Leu	Glu	Ala	
83				205					210					215			
85	gaa	gaa	tat	gtt	cct	atc	ccc	aaa	ggt	gaa	gtc	cat	aag	aaa	aaa	gaa	783
86	Glu	Glu	Tyr	Val	Pro	Ile	Pro	Lys	Gly	Glu	Val	His	Lys	Lys	Lys	Glu	
87			220					225					230				
89	ata	gtg	cag	gat	gtc	aca	ctt	cat	gac	ctt	gat	gca	gca	aat	gct	cag	831
90	Ile	Val	Gln	Asp	Val	Thr	Leu	His	Asp	Leu	Asp	Ala	Ala	Asn	Ala	Gln	
91			235				240					245					
93	cca	caa	ggt	ggc	caa	gat	att	ttg	tcc	ctt	atg	ggc	cag	atg	atg	aaa	879
94	Pro	Gln	Gly	Gly	Gln	Asp	Ile	Leu	Ser	Leu	Met	Gly	Gln	Met	Met	Lys	
95			250				255				260					265	
97	cca	cga	aag	act	gaa	atc	acc	gaa	aaa	cta	cgc	caa	gaa	att	aat	aag	927
98	Pro	Arg	Lys	Thr	Glu	Ile	Thr	Glu	Lys	Leu	Arg	Gln	Glu	Ile	Asn	Lys	
99				270					275				280				
101	gtg	gta	aat	aga	tat	atc	gat	gaa	gga	att	gca	gag	ctt	gta	cct	ggt	975
102	Val	Val	Asn	Arg	Tyr	Ile	Asp	Glu	Gly	Ile	Ala	Glu	Leu	Val	Pro	Gly	
103				285					290				295				
105	gtt	tta	ttc	att	gac	gag	gtc	cac	atg	ttg	gat	atc	gaa	tgt	ttt	tct	1023
106	Val	Leu	Phe	Ile	Asp	Glu	Val	His	Met	Leu	Asp	Ile	Glu	Cys	Phe	Ser	
107			300					305					310				
109	tat	ctt	aac	cgt	gca	ttg	gag	agc	cca	tta	tca	cca	att	gtg	ata	ctt	1071
110	Tyr	Leu	Asn	Arg	Ala	Leu	Glu	Ser	Pro	Leu	Ser	Pro	Ile	Val	Ile	Leu	
111			315				320					325					
113	gct	acg	aat	agg	gga	ata	tgt	aat	gta	aga	gga	act	gat	atg	aca	agt	1119
114	Ala	Thr	Asn	Arg	Gly	Ile	Cys	Asn	Val	Arg	Gly	Thr	Asp	Met	Thr	Ser	
115			330				335				340					345	
117	cca	cat	ggt	ata	cca	gtg	gat	ctt	cta	gat	agg	ttg	gtg	att	att	cgg	1167
118	Pro	His	Gly	Ile	Pro	Val	Asp	Leu	Leu	Asp	Arg	Leu	Val	Ile	Ile	Arg	
119				350					355				360				
121	aca	gag	aca	tat	ggc	cct	act	gag	atg	ata	cag	ata	ttg	gct	atc	cga	1215
122	Thr	Glu	Thr	Tyr	Gly	Pro	Thr	Glu	Met	Ile	Gln	Ile	Leu	Ala	Ile	Arg	
123				365					370				375				
125	gca	caa	gtg	gag	gac	att	gat	atg	gat	gaa	gaa	agt	ctt	gct	tat	tta	1263
126	Ala	Gln	Val	Glu	Asp	Ile	Asp	Met	Asp	Glu	Glu	Ser	Leu	Ala	Tyr	Leu	
127			380					385					390				
129	ggc	gag	atc	gga	cag	cag	aca	tct	tta	aga	cat	gct	att	caa	ttg	ata	1311
130	Gly	Glu	Ile	Gly	Gln	Gln	Thr	Ser	Leu	Arg	His	Ala	Ile	Gln	Leu	Ile	

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131      395      400      405      1359
133 tca cct gcc agc gtg gtc tca aag act aat gga aga gag aaa ata tgc
134 Ser Pro Ala Ser Val Val Ser Lys Thr Asn Gly Arg Glu Lys Ile Cys
135 410      415      420      425      1407
137 aag gct gat ctc gag gaa gtc agt ggg ctc tat ttg gat gcc aaa tcc
138 Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser
139      430      435      440      1449
141 tgg gct cgg ctg ctc cag gag caa caa gaa aga tac atc acc
142 Ser Ala Arg Leu Leu Gln Glu Gln Glu Arg Tyr Ile Thr
143      445      450      455
145 tagatttgga tcacctgtgc tggaagtctc gaagagaatg tagttgccag ctcgaaagtc 1509
146 atctagttaa ttgatctgct tcacaggtct tggagcgagc acatttcggg ggggacggct 1569
147 tgaattttgc agtgcctgct tgtgttagtc tccagagaag acttggtacc ggcattattgc 1629
148 ctgttcacgc actgttcgct gattagattg gtcaccggcg caggaattgc cgtgtgtgtt 1689
149 ttttatcttg ctcatcggtg tccggaatct gtgcctccac gggttgtatt ggcccgaacc 1749
150 ctatctttgt aaccatggat aatggatagc attcttacag aatgcaactt gcatggcttt 1809
151 wttwaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1845
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 455
155 <212> TYPE: PRT
156 <213> ORGANISM: Zea mays
158 <400> SEQUENCE: 2
159 Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile Ala
160 1      5      10      15
161 Thr His Thr His Ile Lys Gly Leu Gly Leu Asp Ala Asn Gly Met Ala
162 20      25      30
163 Ile Ala Leu Ala Ala Gly Phe Val Gly Gln Ser Ala Ala Arg Glu Ala
164 35      40      45
165 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg
166 50      55      60
167 Ala Val Leu Leu Val Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
168 65      70      75      80
169 Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met
170 85      90      95
171 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
172 100      105      110
173 Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys
174 115      120      125
175 Glu Val Tyr Glu Gly Glu Val Thr Glu Leu Ser Pro Glu Glu Ala Glu
176 130      135      140
177 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
178 145      150      155      160
179 Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile
180 165      170      175
181 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
182 180      185      190
183 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
184 195      200      205
185 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro

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186      210      215      220
187 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
188 225      230      235      240
189 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
190      245      250      255
191 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
192      260      265      270
193 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
194      275      280      285
195 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
196      290      295      300
197 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
198      305      310      315      320
199 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
200      325      330      335
201 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
202      340      345      350
203 Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr
204      355      360      365
205 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Asp Ile Asp
206      370      375      380
207 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
208      385      390      395      400
209 Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser
210      405      410      415
211 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
212      420      425      430
213 Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu
214      435      440      445
215 Gln Gln Glu Arg Tyr Ile Thr
216      450      455
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 1912
220 <212> TYPE: DNA
221 <213> ORGANISM: Zea mays
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (94)...(1458)
227 <400> SEQUENCE: 3
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229 acagagagcg cataaccggc ggcgttggcg gcg atg agg atc gag gag gtg cag 114
230      Met Arg Ile Glu Glu Val Gln
231      1      5
233 tcg acc tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga 162
234 Ser Thr Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly
235      10      15      20
237 ctc ggc ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc 210
238 Leu Gly Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe
239      25      30      35

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241	gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg	258
242	Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met	
243	40 45 50 55	
245	att cgc cag aag aag atg gcc ggc cgc gcg gtg ctc ctt gcg ggt ccg	306
246	Ile Arg Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Ala Gly Pro	
247	60 65 70	
249	ccc gcc acg ggc aag acg gcg cta gcg ctc gcc ata gcc cag gag ctc	354
250	Pro Ala Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu	
251	75 80 85	
253	ggc agc aag gtc cct ttc tgt cct atg gta gga tca gaa gtg tac tcc	402
254	Gly Ser Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser	
255	90 95 100	
257	tcg gag gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct	450
258	Ser Glu Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala	
259	105 110 115	
261	ata ggt ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt	498
262	Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val	
263	120 125 130 135	
265	act gaa ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca	546
266	Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala	
267	140 145 150	
269	aaa agc att agc cat gta atc atc agc tta aag act gtt aaa ggg act	594
270	Lys Ser Ile Ser His Val Ile Ile Ser Leu Lys Thr Val Lys Gly Thr	
271	155 160 165	
273	aag caa ctg aag tta gat tct tca att tat gat gct ctg atc aag gaa	642
274	Lys Gln Leu Lys Leu Asp Ser Ser Ile Tyr Asp Ala Leu Ile Lys Glu	
275	170 175 180	
277	aag gtg gca gtg ggt gat gtt ata tac atc gaa gca aat agt gga gca	690
278	Lys Val Ala Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala	
279	185 190 195	
281	gtg aaa aga gtt ggt aga tgt gat tct ttt gct aca gaa tac gat ctt	738
282	Val Lys Arg Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu	
283	200 205 210 215	
285	gaa gct gaa gag tat gtt cct atc ccc aaa ggt gaa gtc cat aag aaa	786
286	Glu Ala Glu Glu Tyr Val Pro Ile Pro Lys Gly Glu Val His Lys Lys	
287	220 225 230	
289	aaa gaa att gtg cag gat gtc aca ctt cat gac ctt gat gca gca aat	834
290	Lys Glu Ile Val Gln Asp Val Thr Leu His Asp Leu Asp Ala Ala Asn	
291	235 240 245	
293	gct cag cca caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg	882
294	Ala Gln Pro Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met	
295	250 255 260	
297	atg aaa cca cga aag act gaa atc acc gaa aaa cta cgc caa gaa att	930
298	Met Lys Pro Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile	
299	265 270 275	
301	aat aag gtg gta aat aga tat atc gat gaa gga att gca gag ctt gta	978
302	Asn Lys Val Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val	
303	280 285 290 295	
305	cct ggt gtt ttg ttc att gat gag gtc cac atg ttg gat atc gaa tgt	1026

VERIFICATION SUMMARY

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Input Set : A:\1121SEQLIST.TXT

Output Set: N:\CRF3\06192000\I589510.raw

OK
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date